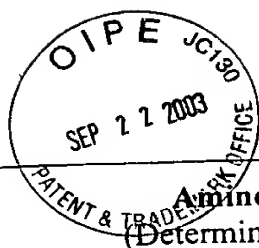


EXHIBIT 1



Amino Acid Sequence Homology Between Heat Shock Proteins
(Determined Using BLAST 2.2.3 (<http://www.ncbi.nlm.gov/blast/bl2seq>))

		% Identical Amino Acids	% Similar Amino Acids	Comments
GroEL (<i>E. coli</i>)	HSP60 (human)	50	71	
Cpn10 (human)	GroES (<i>E. coli</i>)	38	60	
Cpn10 (human)	GroEL (<i>E. coli</i>)			No Significant Similarity Found
Cpn10 (human)	Hsp70 (human)			No Significant Similarity Found
Cpn10 (human)	Hsp90 (human)			No Significant Similarity Found
Cpn10 (human)	Gp96 precursor (human)			No Significant Similarity Found
Hsp90 (human)	Gp96 precursor (human)	47	65	
Hsp90 (human)	GroEL (<i>E. coli</i>)			No Significant Similarity Found
Hsp90 (human)	HSP60 (human)			No Significant Similarity Found
Hsp90 (human)	Hsp70 (human)			No Significant Similarity Found
Cpn10 (human)	Hsp60 (human)			No Significant Similarity Found
Hsp60 (human)	GroES (<i>E. coli</i>)			No Significant Similarity Found
Hsp60 (human)	Hsp70 (human)			No Significant Similarity Found
Hsp60 (human)	Gp96 precursor (human)			No Significant Similarity Found
Hsp70 (human)	GroES (<i>E. coli</i>)			No Significant Similarity Found
Hsp70 (human)	Gp96 precursor (human)	24	41	

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Blast 2 Sequences results

PubMed

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Taxonomy

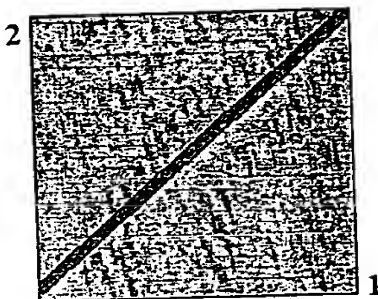
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☐ ALPH

Sequence 1 gi 1790586 GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein [Escherichia coli.K12] Length 548 (1..548)

Sequence 2 gi 306890 chaperonin (HSP60) Length 573 (1..573)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 548 bits (1413), Expect = e-155
Identities = 278/548 (50%), Positives = 396/548 (71%), Gaps = 4/548 (0%)

Query: 3 AKDVKFGNDARVKMLRGVNVVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIEL 62
Sbjct: 27 AKDVKFG DAR ML+GV++LADAV VT+GPKGR V++++ +G+P +TKDGV+VA+ I+L
Query: 63 EDKFENMGAQMVEVASKANDAAGDGTITATVLAQAIITEGLKAVAAGMNPMDLKRIGIDK 122
Sbjct: 87 KDKYKNIGAKLVQDVANNTNEEAGDGTITATVLAARSIAKEGFEKISKGANPVEIRRGVML 146
Query: 123 AVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLI AEAMDKVGKEGVITVEDGTG 182
Sbjct: 147 AVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKT 206
Query: 183 LQDELDVVEGMQFDRGYLSPYFINKPETGAVELES PFILLADKKISNIREMLPVLEAVAK 242
Sbjct: 207 LNDELEIIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANA 266
Query: 243 AGKPLLIIEAEDVEGEALATLVVNTMRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVIS 302
Sbjct: 267 HRKPLVIIIEADVGEALSTLVNRLKVGLQVVAVKAPGFGDNRNKQLKDMAIATGGAVFG 326
Query: 303 EE-IGMELEKATLEDLGQAKRVVINKDTTITIIDGVGEEAAIQGRVAQIRQQIEEATSDYD 361
Sbjct: 327 EEGLTLNLEDVQPHDLGKVGEVIVTKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYE 386

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>

7/29/2002

Query: 362 REKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGVVAGGGVALIR 421
+EKL ER+AKL+ GVAV+KVG ++VE+ EKK RV DAL+ATRAAVEEG+V GGG AL+R
Sbjct: 387 KEKLNERLAKLSDGVAVLKVGGSVDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLR 446

Query: 422 VASKLADLRGQONEDQNVGIKVALRAMEAPLRQIVLNCGEPSVVANTVKGGDGNYGYNAA 481
L L NEDQ +GI++ R ++ P I N G E S++ + GY+A
Sbjct: 447 CIPALDSLTPANEDQKIGIEIIRKTLKIPAMTIKAGVEGSLIVEKIMQSSSEVGYDAM 506

Query: 482 TEEYGNMIDMGILDPTKVTRSAQYAASVAGLMITTECMVTDLPKNDA-ADLGAAGGMGG 540
++ NM++ GI+DPTKV R+AL AA VA L+ T E +VT++PK + +GA GGMG
Sbjct: 507 AGDFVMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVTETIPKEEKDPGMGAMGGMG- 565

Query: 541 MGGMGGM 548
GGMGG M
Sbjct: 566 -GGMGGGM 572

CPU time: 0.13 user secs. 0.03 sys. secs 0.16 total secs.

Lambda	K	H
0.313	0.132	0.351

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 3820

Number of Sequences: 0

Number of extensions: 355

Number of successful extensions: 4

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 548

length of database: 327,972,341

effective HSP length: 128

effective length of query: 420

effective length of database: 251,365,749

effective search space: 105573614580

effective search space used: 105573614580

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 75 (33.5 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

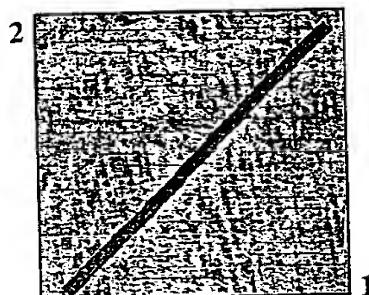
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Align

Sequence gi heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102 (1..102)
 1 4504523

Sequence gi GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, Length 97 (1..97)
 2 1790585 suppressing its ATPase activity [Escherichia coli K12]



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 64.3 bits (155), Expect = 8e-11
 Identities = 34/88 (38%), Positives = 54/88 (60%), Gaps = 1/88 (1%)

Query: 11 PLFDRVLVERSAETVTKGGIMLPEKSQGVLTQATVVAVGSGSKGKGGEIQPVSVKVGDK 70
 PL DRV+V+R ET + GGI+L + K + V+AVG+G + GE++P+ VKVGD
 Sbjct: 5 PLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNRILENGEVKPLDVKVGDI 64

Query: 71 VLLPE-YGGTKVVLDDKDYFLFRDGDIL 97
 V+ + YG +D+++ + + DIL
 Sbjct: 65 VIFNDGYGVKSEKIDNEEVLIMSESDIL 92

CPU time: 0.02 user secs. 0.05 sys. secs 0.07 total secs.

Lambda K H
 0.313 0.136 0.357

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 119
 Number of Sequences: 0
 Number of extensions: 13

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>

7/29/2002

Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 97
length of database: 327,972,341
effective HSP length: 73
effective length of query: 24
effective length of database: 81,147,807
effective search space: 1947547368
effective search space used: 1947547368
T: 9
A: 40
X1: 16 (7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 60 (27.7 bits)




Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ 

Sequence	gi	heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens]	Length	102
1	<u>4504523</u>			

Sequence	gi	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock	Length	548
2	<u>1790586</u>	protein [Escherichia coli K12]		

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ **Align**

Sequence 1 gi [4504523](#) heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102

Sequence 2 gi [292160](#) heat shock protein 70 Length 701

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ **Align**

Sequence 1 gi 4504523 heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102Sequence 2 gi 32488

Length 732

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: [11](#) gap extension: [1](#)x_dropoff: [50](#) expect: [10.000](#) wordsize: [3](#) Filter ☐ [Ala](#)Sequence 1 gi [4504523](#) heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102Sequence 2 gi [15010550](#) heat shock protein gp96 precursor [Homo sapiens] Length 782**No significant similarity was found**



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

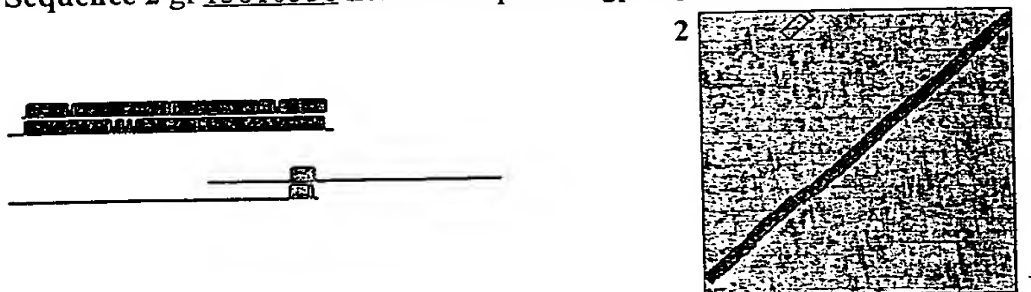
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☐ Align

Sequence 1 gi 32488

Length 732 (1 .. 732)

Sequence 2 gi 15010550 heat shock protein gp96 precursor [Homo sapiens] Length 782 (1 .. 782)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 637 bits (1643), Expect = 0.0
 Identities = 344/729 (47%), Positives = 479/729 (65%), Gaps = 27/729 (3%)

```

Query:          15  EEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDP SKL
                  E+ E FAFQAE+ ++M LIIN+ Y NKEIFLRELISN+SDALDKIR  +LTD + L
Sbjct:          50  EKSEKFAFQAEVNRMMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENAL
heat shock protein gp96 50  *****

Query:          75  ELHINLIPNKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFM---EALQAGA
                  EL + + +K+ L + DTG+GMT+ +L+ NLGTIAKSGT F+ EA + G
Sbjct:          110 ELTVKIKCDKEKNLLHVTDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQEDGQ
heat shock protein gp96 110 *****

Query:          130  MIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTK
                  +IGQFGVGFYSA+LVA+KV V +KHN+D Q+ WES + + G +GRGT
Sbjct:          170  LIGQFGVGFYSAFLVADKVIIVTSKHNDTQHIWESDSNEFSVIADPRGNTLGRGTT
heat shock protein gp96 170 *****

Query:          190  LKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVEKERDKEVSDDEAEKEDKEEEK
                  LKE+ ++YLE IK +VKK+SQFI +PI ++ K E E+ +EEE
Sbjct:          230  LKEEASDYLELDTIKQLVKKYSQFINFPIYVWSSKT-----ETVEEPMEEEEE
heat shock protein gp96 230 *****

Query:          250  KESEDKPEIEDVGSDEEEKKDGDKKKKKKIKEYIDQEELNKT KPIWTRNPDDIT
                  KE D ++ +EEEE+K K K KK+++ D E +N KPIW R ++
Sbjct:          282  KEESD----DEAAVEEEEEK---KPKTKKVEKTVWDWELMNDIKPIWQRP SKEVE
heat shock protein gp96 282 *****
  
```

Query: 310 GEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFVPRRAPFDLFEN--RKKKNNIKL
 FYKS + + +D +A HF+ EG++ F+++LFVP AP LF+ KK + IKL
 Sbjct: 335 KAFYKSFSKESDDPMAYIHFTAEGEVTFKSILFVPTSAPRGLFDEYGSKKSDYIKL
 heat shock protein gp96 335 *****

Query: 368 VFIMDNCEELIPEYLNFIIRGVVDSDDLPLNISREMLQQSKILKVKIRKNLVKKCLEL
 VFI D+ +++P+YLN++GVVDS+DLPLN+SRE LQQ K+LKVIRK LV+K L++
 Sbjct: 395 VFIPDDFHDMMPKYLNFKGVVDSDDLPLNVSRETLLQKHLLKVKIRKKLVKRLTDM
 heat shock protein gp96 395 *****

Query: 428 AEDKENYKKFYEQFSKNIKLGIHEDSQNRKKLSELLRYYTSASGDEMVSLLKDYCTR
 A+DK N F+++F NIKLG+ ED NR +L++LLR+ +S ++ SL Y R
 Sbjct: 455 ADDKYN-DTFWKEFGTNIKLGVIEDHSNRTLAKLLRFQSSHHPTDITSLDQYVER
 heat shock protein gp96 455 *****

Query: 488 QKHIYYITGETKDQVANSFAVERLRKHGLEVIYMIPIDEYCVQQLKEFEGKTLVS
 Q IY++ G ++ + +S FVERL K G EVIY+ EP+DEYC+Q L EF+GK +
 Sbjct: 514 QDKIYFMAGSSSRKEAESSPFVERLLKKGVEVIYLTPEVDEYCIQALPEFDGKRFQN
 heat shock protein gp96 514 *****

Query: 548 GLELPEDEEEKKKQEEKTKFENLCKIMKD-ILEKKVEKVVSNNRLVTSPCCIVTS
 G++ E E+ K+ +E + +FE L MKD L+ K+EK VVS RL SPC +V S
 Sbjct: 574 GVKFDESEKTKESREAVEKEFEPLLNWMKDKALKDKIEKAVVSQRLTESPCALVAS
 heat shock protein gp96 574 *****

Query: 607 TANMERIMKAQAL---RDNSTMGYMAAKKHLEINPDHSIIETLRQKAEADKNDKSV
 + NMERIMKAQA +D ST Y + KK EINP H +I + + + D++DK+V
 Sbjct: 634 SGNMERIMKAQAYQTGKDISTNYASQKKTFEINPRHPLIRDLMLRIKEDDDKTV
 heat shock protein gp96 634 *****

Query: 664 ILLYETALLSSGFSLEDPOQTHANRIYRMIKLGIGIDEDDPTADDTSAAVTEEMPPL
 ++L+ETA L SG+ L D + + +RI RM++L L ID D ++ E
 Sbjct: 694 VVLFTATLRSGYLLPDTKAYGDRIERMLRLSLNIDPDAKVEEPEEPEETAEDT
 heat shock protein gp96 694 *****

Query: 724 DTSRMEEVD 732
 + EE+D
 Sbjct: 754 EQDEDEEMD 762
 heat shock protein gp96 754 *****

Score = 35.0 bits (79), Expect = 4.6
 Identities = 20/61 (32%), Positives = 34/61 (54%), Gaps = 2/61 (3%)

Query: 208 KKHSQFIGYPITLFVEKERDKEVSDDEAEKEDKEEKEKEEKESEDKPEIEDVGS
 K + I + L + + D +V ++ EE E+ E+ ++ ++ ED E DVG+
 Sbjct: 712 KAYGDRIERMLRLSLNIDPDAKVEEPEEPEETAEDTTEDTEQDED--EEMDVGT
 heat shock protein gp96 712 *****

Query: 268 E 268
 E
 Sbjct: 770 E 770
 heat shock protein gp96 770 *

CPU time: 0.27 user secs. 0.09 sys. secs 0.36 total secs.

Lambda K H
 0.312 0.132 0.361

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12,881

Number of Sequences: 0

Number of extensions: 826

Number of successful extensions: 62

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 14

length of query: 732

length of database: 327,972,341

effective HSP length: 131

effective length of query: 601

effective length of database: 269,277,922

effective search space: 161836031122

effective search space used: 161836031122

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 77 (34.3 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☐

Sequence
1 gi 32488

Length 732

Sequence gi GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock
2 1790586 protein [Escherichia coli K12]

Length 548

No significant similarity was found



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Sequence 1 gi 32488

Length 732

Sequence 2 gi 306890 chaperonin (HSP60) Length 573

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐

Sequence 1 gi_32488

Length 732

Sequence 2 gi_292160 heat shock protein 70 Length 701

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ **AL-50**

Sequence 1 gi 4504523 heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102

Sequence 2 gi 306890 chaperonin (HSP60)

Length 573

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: gap extension:

x_dropoff: expect: wordsize: Filter ☐ [Align](#)

Sequence
1 [gi_306890](#) chaperonin (HSP60)

Length 573

Sequence [gi_1790585](#) GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP,
2 suppressing its ATPase activity [Escherichia coli K12]

Length 97

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: gap extension: x_dropoff: expect: wordsize: Filter ☐ [Align](#)Sequence 1 gi [306890](#) chaperonin (HSP60) Length 573Sequence 2 gi [292160](#) heat shock protein 70 Length 701

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: gap extension: x_dropoff: expect: wordsize: Filter ☐ [Help](#)Sequence 1 gi [306890](#) chaperonin (HSP60)

Length 573

Sequence 2 gi [15010550](#) heat shock protein gp96 precursor [Homo sapiens] Length 782

No significant similarity was found

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

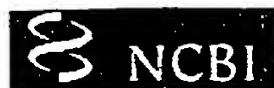
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]Matrix: BLOSUM62 gap open: 11 gap extension: 1x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Sequence
1 gi 292160 heat shock protein 70

Length 701

Sequence gi GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP,
2 1790585 suppressing its ATPase activity [Escherichia coli K12]

Length 97

No significant similarity was found



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

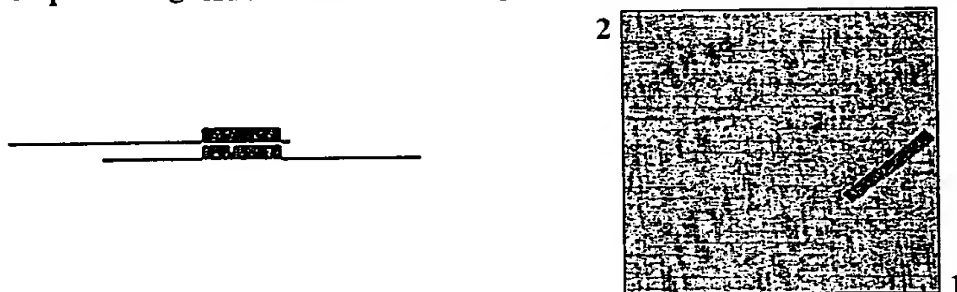
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.00** wordsize: **3** Filter ☐ **Align**Sequence 1 gi 292160 heat shock protein 70

Length 701 (1 .. 701)

Sequence 2 gi 15010550 heat shock protein gp96 precursor [Homo sapiens] Length 782 (1 .. 782)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 39.3 bits (90), Expect = 0.23

Identities = 44/180 (24%), Positives = 75/180 (41%), Gaps = 7/180 (3%)

```

Query:          502 KSEENEETDQNAKEEEKMQVDQEEPHVEEQQQQTPAENKAESEEMETSQAGSK
                  K+E  EEPME ++ AK EEK + D E  EE++++ P  K E  +
Sbjct:          264 KTETVEEPMEEEEAAK-EEKEESDDEAAVEEEEEEEKPKTKKVEKTVWDWELMNDI
heat shock protein gp96 264 *****
Query:          562 DQPPQCQEGKSEDQYCGPANRESAIWQIDREMLNLYIENEGKMIMQDKLEKERNDA
                  +P + E  ED+Y  A +S  + D M ++ EG++ + L  +
Sbjct:          323 QRPSKEVE---EDEY--KAFYKSFSKESDDPMAYIHFTAEGEVTFKSILFVPTSAP
heat shock protein gp96 323 *****
Query:          622 EEYVYEMRDKLSGEYEKFVSEDDRNSFTLKLEDTENWLYEDGEDQPKQVYVDKLA
                  +EY + D +  +  DD +  K +  +  D +D P V + L +
Sbjct:          378 DEYGSKKSDYIKLYVRRVFIPDDFHDMMPKYLNFKGVV-DSDDLPLNVSRETQQ
heat shock protein gp96 378 *****

```

CPU time: 0.23 user secs. 0.04 sys. secs 0.27 total secs.

Lambda	K	H
0.314	0.131	0.369

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 9115
Number of Sequences: 0
Number of extensions: 564
Number of successful extensions: 9
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 6
length of query: 701
length of database: 327,972,341
effective HSP length: 131
effective length of query: 570
effective length of database: 266,682,288
effective search space: 152008904160
effective search space used: 152008904160
T: 9
A: 40
X1: 16 (7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.9 bits)
S2: 76 (33.9 bits)